



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Clinton, Gail M., Doherty, Joni Kristin, and Adelman, John P.

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIS WRIGHT TREMAINE

(B) STREET: 1501 Fourth Avenue, 2600 Century Square

(C) CITY: Seattle

(D) STATE: Washington

(E) COUNTRY: U.S.A.

(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: PC compatible

(C) OPERATING SYSTEM: Windows95

(D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/506,079

(B) FILING DATE: February 16, 2000

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Oster, Jeffrey B.

(B) REGISTRATION NUMBER: 32,585

(C) REFERENCE/DOCKET NUMBER: 49321-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206 628 7711

(B) TELEFAX: 206 628 7699

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	Xaa
				5					10					15	
Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	Arg	Pro
			20					25					30		
Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	Ala	Pro	Leu
		35					40					45			
Ser	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val	Gly	Arg	Gly	Xaa
	50					55					60				
Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	Arg	Tyr	Glu	Gly	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu
				5					10					15	
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Cys	Lys
			20					25					30		
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His
			35				40					45			
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr
	50					55					60				
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
	65				70					75					
Gln	Gly	Tyr	Val	Leu	Cys	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
80					85				90					95	
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
			100					105						110	
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Arg	Arg	Thr	Thr	Pro
			115				120						125		
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
		130				135						140			
Leu	Thr	Glu	Cys	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
	145					150					155				
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
160				165					170					175	
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
			180					185						190	
His	Pro	Cys	Ser	Pro	Cys	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser

195 200 205
 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 210 215 220
 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 225 230 235
 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 240 245 250 255
 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
 260 265 270
 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
 275 280 285
 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
 290 295 300
 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
 305 310 315
 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
 320 325 330 335
 Pro Cys Ala Arg Val Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala
 340 345 350
 Val Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu
 355 360 365
 Ser Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu
 370 375 380
 Pro Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser
 385 390 395
 Val Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
 400 405 410 415
 Arg Tyr Glu Gly

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

- cont-*
- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGT WCC CAC TCA CYG CYC CCG AGG CCA GCT GCA GTT CCT GTC CCT 45
Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro
5 10 15

CWG CGC ATR CAG CCT GNC CCA GCC CAC CCT GTC CTA TCC TTC CTC 90
Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu
20 25 30

AGA CCC TCT TGG GAC MTA GTC TCT GCC TTC TAC TCT CTA CCC CTG 135
Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu
35 40 45

GCC CCC CTC AGC CCT ACA AGT GTC CST ATA TCC CCT GTC AGT GTG 180
Ala Pro Leu Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
50 55 60

GGG AGG GGC CYG GAC CCT GAT GCT CAT GTG GCT GTT SAC CTG TCC 225
Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
65 70 75

CGG TAT GAA GGC TGA 240
Arg Tyr Glu Gly